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FIGURE 418

MTKARLFRLWLVLGSVFMILLIIIVYWDSAGAAHFYLMHTSFSRPHTGPPPLPTPGPDRDRELTAD
SDVDEFLDKFLSAGVKQSDLPKRETEQPPAPGSMEEESVRGYDWSPRDARRSPDQGRQQAERRS
VLRGFCANSSLAFTPTEKRAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSL
LHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPFVRLI
SAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKL
APFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLQLQLQVDRQLRFPPSYRNRTASSWEE
DWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:**Signal peptide:**

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

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FIGURE 419

GGCACGAGGGCTGAACCCAGCGCGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG
GCTGCCAGGAAGGAGACGCCTTCTCTGAGTCTTGGATCTTTCTTCCTTCTGGAAATCTTTGACT
GTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGCTGA
AGTCTCAGTTCTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATCATCA
ACACCATTGAGCTCTTCACTCTCTCTCTCTGCCCCATTAACAAGCAGCTCTTCCGGAAGATCA
ACTGCAGACTGTCTATTGCACTCTCAAGCCAGCTGGTGATGTCTGTGGAGTGGTGGTCCGGGCA
CGGAATGCACCATCTTCACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAATGCCATCG
TGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGAACGCTTGTG
GGCTGTTAGGGGGCTCCAAGGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCT
GGATGTGGTACTTACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGATCGCAAGACGG
TTGCCACCAGTTTGACGACCTTCGGGACTACCCCGAGAAGTATTTTTCTCTGATTCACTGTG
AGGGCACAGGTTACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCCGGGCCAAGGGGC
TGCCCTCGCCTCAAGCATACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCT
TGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAATAATGAAAATCCAA
CACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATGTTAGGAGGATCCAC
TGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAGCTCTACCAGGAGA
AGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGAGACGCCCATGGTGCCCC
CCCGCGGGCCCTGGACCTCGTGAACCTGGCTGTTTGGGGCTCGCTGGTGTCTTACCCTTTCT
TCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCTCTG
TCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGTGACGGAATTGACAAGGGCT
CTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACTTGACTCAGGGAGGTGTCCACAT
CCGAAGGGAACCTTGGGGAACTGGTGGCCTCTGCATATCCTCCTTAGTGGGACACGGTGACAA
AGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT
CTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTTTTTTCCCATGTGCTTTAGTGGGC
TTTGTTTTCTTTTGTGCGAGTGTGTGTGAGAAATGGCTGTGTGGTGAGTGTGAACCTTTGTTC
TGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGGACCGAAGGGGACA
AGTTCCCCCTTTCATCCTTTGGTGCTGAGTTTTCTGTAACCCCTGGTTGCCAGAGATAAAGTGA
AAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAATTAAGTGCTTTTCT
GGGTCAAAAAAAAAA

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FIGURE 420

MDLAGLLKSQFLCHLVFCYVFIAASGLIINTIQLF TLLLWPINKQLFRKINCRLSYCISSQLVM
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGGSKVLAKKEL
AYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHEISM
QVARAKGLPRLKHHLLPRTKGF AITVRS LRNVVSAVYDCTLNFRNNENPTLLGVLNGKKYHAD
LYVRRIPLEDI PEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVNWLFWA
SLVLYPFFQFLVSMIRSGSSLTASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDSKQKLND

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FIGURE 421

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCATC
GCCATGACACACCACAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGCCC
TGGGGACGCTGGGTGCATCGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTGGGTCAAC
ACAGTCCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCGCG
CTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGCGCTGGGTGCC
CTGAAGGAGGAGGTGCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTGCAGACC
ACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCGGGAA
CTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACGTCCGCACT
GAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCGTGCCCCACG
TCGTGGCTGTCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGACGTGGGCGGCG
GCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCTGGATGAGCAG
GGCTTCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCGCTGAGGCTGTGCGCCAT
CTGGGCAAGGTTCAAGGGCTACCAAGTGGGTGGACGGAGTCTCTCTCAGCTTCAGCCACTGGAAC
CAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGCTGCACACGGGGCTG
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACCTGC
TGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCGTATCCTGGGGCTGCTCA
CCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCTCATCCACGCTGCTGAG
TCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCAGTGCCTGGGCTCTGGGACCTCCA
TGCCGACCTCATCTAACTCCACTCACGCAGACCCAACCTAACCTCCACTAGCTCCAAAATCC
CTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAACCAAGGTTAGGTGACTGAGG
ACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGAAGCTGTTTTTGACGCTGAGG
AAGCATCAATAAATATTTGAGAAATGAAAAA

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FIGURE 422

MDTTRYSKWGSSEEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAAL
LDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALREL
RERVTTQGLAEAGRGREDVRETELFRALEAVRLQNNSCPECPTSWLSFEGSCYFFSVPKTTWAAA
QDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFSHWNQ
GEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:**Type II transmembrane domain:**

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

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FIGURE 423

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCCTCTCCGCTTCCTTGAAAAACCCGGCGGGC
GAGCGAGGCTGCGGGGCCGGCCGCTGCCCTTCCCCACACTCCCGCGCCGAGAAGCCTCGCTCGGC
GCCAACATGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGATCGC
GGCTGTGGCGCGACGGCAGGCCCGAGGAGGCGCGCTGCCCGGAGCAGAGCCGGGTCCA
GCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTTTACGC
CCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAAGAATGGTG
AATACTTCAGATCAGTGTGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAAGTGGCCGCTT
CTTTGTCACTCTCCAGCATTTTTTCATGCAAGGATGGGATATTCGCGCTTATCGTGG
CCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATCAGTCGAGCC
TCTGACTGGCTGGAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTCTTTTAGCAT
CTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGAATTCCTGCTTGGTG
TTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTGGCCTTTTTATGGGCTGGTCTTGGT
GGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTTATCTGAGCGTTCTGAGCAGAA
TCGGAGATCAGAGGAGGCTCATAGACTGAACAGTTGCAAGATGCGGAGGAGGAAAAAGATGA
TTCAATGAAGAAGAAAAACAAGACAGCCTTGATAGATGATGAAGAAGAGAAAGAGATCTTG
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAATTGGCTGCTGGTGTGGATGAGGA
GAGAAGTGAGGCCAATGATCAGGGGCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTAGA
GCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCTGCCAGCTGACACAGAGGTGGTGGA
AGACTCCTTGAGGCAGCGTAAAGTCAGCATGCTGACRAGGAGCTGTAGATTAAATGATGCGT
TTTCAAGAATACACACCAAAACAATATGTGAGCTTCCCTTTGGCCTCGAGTTTGTACCAATC
CTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCTCTCTAGTCATTTGGTCTCATG
GCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGTGACAAATCAGGATATAGAAAAAC
AAACGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAACAAGTTCATTTACTTAGGGGTCA
GAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCTTAATCAGCACCTTCCAGAGACAAGGCTGC
AGGCCCTGTGAAATGAAGCCAAGCAGGAGCCTTGGCTCCTGAGCATCCCCAAAGTGTAAAGT
AGAAGCCTTGATCCTTTTTCTGTGTAAAGTATTTATTTTGTCAAATTCGAGGAAACATCAG
GCACCACAGTGCATGAAAAATCTTTCACAGCTAGAAATGAAGGGCCTTGGGTATAGAGAGC
AGCTCAGAAGTCATCCAGCCCTCTGAATCTCTGTGCTATGTTTTATTTCTTACCTTTAAT
TTTCCAGCATTTCCACCATTGGGCATTGAGCTCTCCACACTTTCATATTATCTCTTGGTCA
GAGGACTCCAATAACAGCCAGGTTTACATGAACGTGTGTTGTTTCTTCTGACCTAAGGGGTTT
AGATAATCAGTAACCATAAACCCCTGAAGCTGTGACTGCCAAACATCTCAATGAAATGTTGTG
GCCATCAGAGACTCAAAAGGAAGTAAGGATTTTACAAGACAGATTAATAAAAAAATGTTTGT
CCAAATATAGTTGTTGTTGATTTTTTTTAAAGTTTTCTAAGCAATTTTTTCAAGCCAGAAG
TCCTCTAAGCTCTGGCAGTACAGGTAGTCTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTT
ATCTCAAGGGGTTCCCTGGGTCTGAACTACTTTAATAATACTAAAAAACCACTTCTGATTT
TCCTTCAGTGATGTCCTTTTGGTGAAGAATTAATGAACCTCAGTACTGAAAGTGAAAGATT
TGATTTTGTTCATCTCTGTAATCTTCCAAGAATTATATCTTTGTAATCTCTCAATCT
CAATCTACTGTAAGTACCCAGGGAGGCTAATTTCTTT

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FIGURE 424

MAGGRCGPQLTALLAAWIAAATAAGPEEAALPPEQSRVQPMNTASNWTLMMEGEWMLKFYAPW
CPSCQQTDSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFFRRYRGG
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAWCSY
VFFVIATLVFGLFMGLVVLVVISFCFYVPLPRHLSESRSEQNRRSEEAHRAEQLQDAEEEEKDDSN
EEENKDSLVDDEEEKEDLGDEDEAEEEEEEDNLAAGVDEERSEANDQGPPGEDGVTRREEVEPE
EAEEGISEQPCPADTEVVEDSLRQRKSHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

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FIGURE 425

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACC AATCCCGTGCGCCGGG
 CTGGGCCGTGCGAGAGTGGCTGTGCTTCTCTCTGCACGCCGGTGTGGGCTCGGCCAGGGCGGGGCTCCGCCGCCA
 GGGTTTCAGGATGGGGGGTAGTCAAGGAAGCGACCCGCCGATGGCAAGGTATATTTTGTGGAAATGAAAAGGA
 AGTATTAGAAATGAGCTGAGACACCTTACAGATTAAATTTTGGGGACAGATTGTGATGCTTATTACCCCT
 TGAAGTATGTGACAGAAAGTTTCAAATTTGCAATTTACATCACTGGAACACGACGTGAATCTTAAATGTTTAC
 TTAATTCAGAACTGCATAAGAAAGAGAAATGCGAGCTCTGTTAAATAAAGATGACTATATCAGAGACTTGAAGA
 GATCATCTCTCTTTTCTGATAGTGTATATGGCCATTTTATGTGGGCACAGATCAGGATTTTTCAGTCTTCTGG
 AGTGTCCAAAATCGCAAGCAGTAGAGAAATAAGACAAGCTTTCAGAAATTTGGCATTGAGTTAGTATCTTGATAA
 AAAACCCGAATAACCCAAATGCACATGGCGATTTTAAAAAATAATAGAGCATATGAATGACTCAAGATGAAGA
 CTACGGAAGAAAGTATGACAAATATGGAGAAAAGGGAATTCAGGATAATCAAGTGGCCAGTATGAAGCTGGAA
 CTATTATCGTTATGATTTTGGTATTTATGATGATGATCTGAAATCATAACATTTGGAAGAAAGAGAAATTTGATGC
 TGCTGTTAATTTCTGGAGAACTGTGGTTTGTAAATTTTACTCCCGAGGCTGTTACACTGGCATGATTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAAAGTGGATGGGTACTTCGAATTTGGAGCTGTTAAGTGTGGTATGATAGAAT
 GCGTTGCCGAATGAAGAGGATCAACAGCTATCCAGTCTCTTCAITTTTCGGTCTGGATGGCCCCAGTGAATA
 TCATGGAGACAGATCAAAGGAGATTTAGTGAGTTTTCGATGACGATGTTAGAAGTACAGTGACAGAACTTTG
 CACAGGAAATTTTGCACTCCATACAACTGCTTTTGTCTGCTGATTTGGCTGGCTGATCACTTTTGTTCAAA
 AGGAGGAGATTTGTTTGAATCTCAGACACGCACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAA
 AGAAATATTTTGGAGATTAATACATAATCTCCAGATTTTGAAGTACTTTTCGGCAACACCATAGAGGATCGTTT
 GGCTCATCATCGGTGGCTGTTATTTTCAITTTTGGAAAAATGAAATTCAAATGATCTCGAGTGCAAAAACT
 AAAAAGCTCTACTTAAAAATGATCATATTCAGGTTGGCAGGTTTGACTGTTCCCTCGACCCAGACATCTGTAGTAA
 TCTGTATGTTTTCAGCGCTCTTCAGCATTTTAAAGGACAGGAACAAAGAAATGAAATTCATCACTGGAA
 GAAGATCTATATGATATACCTGGCTTTGCCAAAGAAAGTGTGAATCTCATGTTACACCGCTTGGACCTCAAAA
 TTTCCTGGCAATGACAAAGAACCACTGGCTTGTGTATTTTGTGCCCTGTTGCCACCATGTTCAGAGCTTTACT
 ACCAGATTTACGAAGAGCATTAATCTTCTTATGGTCAGCTTAAAGTTTGGTACCATAGATTGTACAGTTCATGA
 GCGCTCTGTAACTATATAACTTCAGGCTTATCCACACAGAGTGGTATTACACAGTCCCAACATTCATGAGTA
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATCTTATGAATCCTTCAGTGGCTCCCTCTAC
 ACCCACCACCTTCAACGAAGTAGTTACACAAAGAAAACACACGAAGTCTGGAGTGTGATTTCTATCTCCGTG
 GTGTCATCCTTGCCAGTCTTAAATGCCGAATGGAAAGAAATGGCCGGACATTAACTGGACTGATCAAGCTGGG
 CAGTATAGATTTGCCAAGCATATCATCTTTTGTGCCAGGAAAAACGTTCAAAGATACCCCTGAGATAAAGATTTT
 TCCCCCAAAATCAAATAAAGCTTATCAGTATCAGAGTACAATGGTGGAAATAGGATGCTTATCCCTGAGAAT
 CTGGGGTCTAGGATTTTACTCAAGTATCCACAGATCTAACACCTCAGACTTCAGTGAAGAAATTTCTCAAGAT
 GAAAAATCATTTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTGCTCAGAATTTGAGCT
 CTGGCTAGGATGATTAAGGAAAAAGTGAAGCTGGAAAAAGTAGACTGCAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGGCTCTCAACCTTTAAGTTTATTTCTACGAAAGACAAAGAGAAATTTTCAAGAAAGACA
 GATGAATACCCAGAGATGAAGAAGCAATCGCTGCCCTAATAAAGTGAAGAAATTTGGAAGCTTCGGAATCAAGGGCA
 GAGGAATAAGGATGAATTTTGAATGTGAAGATGAAGAAAGTTTAAAGAAATCTCAGAGATGACATCAG
 AAGACACCTATTAGAACTTACATTTATGATGCGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA
 GAATATCTACAGCACTGGTGTAAAAGAGGGTCTGCAAACTTTTCTGTAAGAAGGCCGGTTTATAAATATTTTCA
 GATTTGACGGCTATTAATATATGTTTCACACATGAGAACAAGAAATAGAGCTCATCATCTTCTGTTATTGCT
 TTTAAACAACCTTTAAAAAATTTAAAAAGCATCTTAGCTCAGAGCCATACAAAGATGAGCTGGAATCGCTCCATG
 GACCATAGATTGCTGCTCCCTCGACCGGACTATAATGTTTCAGTGGCTGGCTGAACATGAGTTCAGTGTGCT
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTCCCTTCAGCTTTTGGCTGACCTGAAAGAGAGTAACT
 TAGTTTGGTGACTGTTCTCTCTAAAAATGCTATCCCTAACCATATATTATTTATGTTTCTGTTTAAAAACACCAT
 GATGTGGCACACATAAACACCCCTGTTATGCTGATTATATGAGGAGATTTCTTCAATTTGTTTCTTCTCTCA
 AAGTTGCAAAAAATGCTTTTAAATTTTCAACGCGAGAAACAGTGCACGATATGTGTCACACAGTAAAGTACAC
 AAATTTGAGCAACAGTAAAGTGCACAAATCTCTAGTTTGTCTGATCATCCAGGAAACCTGAGGGNAAAAAATTA
 TGAACAAATAACTGGGCATTTGAGAGTATCCATAATATGTTATCAAGTATTAGAGTTCTAATTTTAAAGATATA
 TGTGTTCAAGTATTTTCAAAATTTGCTTTCTATGAAATTTCCCACTGATGATGATTTTGAAGGCATCTAATAT
 TTACATATTTTGCTTTCTGAACCTTTGTTTGACCTGTATCCCTTATTTACATTTGGGTTTTCITTCATGATTTTGG
 TTTTCTCACTCTGTCCAGTCTATTATTATTTCAAAATAGGAAAAATTTACTTACAGGTTTGGTTTCTAGCTATT
 AATGATAGCTGTAGTTATTTCAGTTTACAGTTTACTGTTCAGAGGGCTGCCCTTTTCAGATTAATATTGACATATA
 ACTGAAGTTATTTTTAAAGAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTTTGAATGA
 CTCAGAAATCACAATTTGTGATGAACATGTAGTTGTTTGTATTATAATTCAGAGTGTACAGAAATGGTAAAAAT
 CCAATCAGTCAAAAGAGCTCAATGAATTAAGAGCTTGAACCTTTTCAAAAAAAGAAAAA

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FIGURE 426

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDDQDFYSLLGVSKTASSREIRQAFKKLALKLH
PDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLDNQGGQYESWNYRYDFGIYD
DDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDD
RMLCRMKGVSYPFLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSVTTELWTGNEFVNSIQTA
FAAGIGWLITFCCKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDR
LAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQPSLAVFK
GQGTKEYEIIHHGKKILYDILAFAKESVNSHVTTLGPQNFFANDKEPWLVDFFAPWCPPCRALL
PELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVFVFNQSNIEYEGHSSAEQILEFI
EDLMNPSVVSILTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVG
IDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLGFLPQVSTDLT
PQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDQQAQTCQKAG
IRAYPTVKFYFYERAKRNFQEEQINTRDAKATAALISEKLETLRNQGRNKDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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FIGURE 427

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGACCCCTGACTCTGCAGCCGAACCGGCA
CGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTCTCCCTCTTGA
GTCTTCTTGAGATGATGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGGTAG
CGGCGGCTCTCGGCGGCCACCCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTCAATT
CCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTCTGCAG
TCAGCGCCGCGCGGGAATCCTGTACCGGGCGGGAATAAGTACCAGACCATTGACAACTACC
AGCCGTACCCGTGCGCAGAGGACGAGGAGTGC GGCACTGATGAGTACTGCGCTAGTCCCACCC
GCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACGCTGCATGC
GTCACGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGCTTCTGATCAAA
ATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGATCATAGCACCT
TGGATGGGTATTCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAAAGGACAAGAAG
GTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTAGACACTTCTGGT
CCAAGATCTGTAAACCTGTCTTGAAAGAAGGTCAAGTGTGTACCAAGCATAGGAGAAAAGGCT
CTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCTTGCCGGATACAGA
AAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGAGACACTAAACCAGCT
ATCCAAATGCAGTGAACCTCCTTTTATATAATAGATGCTATGAAAACCTTTTATGACCTTCATC
AACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCATTCCAATAACACCTTCCA
AAAACCTGGAGTGTAAGAGCTTTGTTTCTTATGGAACCTCCCTGTGATTGCAGTAAATTACT
GTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGAACTTTTAATTATTTTCT
AAAGGTGCTGCACCTGCCTATTTTTCTCTTGTATGTAAATTTTGTACACATTGATTGTTAT
CTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTTTCAGCTTATAGTTCTTAAAG
CATAACCCCTTTACCCATTTAATTCTAGAGTCTAGAACGCAAGGATCTCTGGAATGACAAAT
GATAGGTACCTAAATGTAACATGAAAATACTAGCTTATTTTCTGAAATGTACTATCTTAATG
CTTAATTTATATTTCCCTTTAGGCTGTGATAGTTTTTGAATAAAATTTAACATTTAAAAAA
AAAAA

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FIGURE 428

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPLGGAAGHPGSVAVSAA
PGILYPGGNKYQTIIDNYQYPYCAEDEECGTDEYCASPTRGGDAGVQICLACRKRKRRCMRHAM
CCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRRTLSSKMYHTKGQEGSVC
LRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQKDHH
QASNSSRLHTCQRH

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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FIGURE 429

GAGAGGACGAGGTGCCGCTGCCGTGGAGAATCCTCCGCTGCCGTCCGGCTCCCGGAGCCAGCCCC
TTTCCTAACCACACCCAACTAGCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGACCC
CAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCT
CCTGGTAACCTTGGGTTTTTACTCCTGTAACAACGTAAATAACAAGTCTTGCTACAGAGAATAT
AGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGTCTGTTT
CAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAAGGAAGAATTTCCAAA
TGAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCAGAGATA
CAGGATAAGCAAATACCCAAACCTCAAATTTGTTTCGTAATGGGATGATGATGAAGAGAGAATA
CAGGGGTGACGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAGTGACCCCAT
TCAAGAAATTCGGGACTTAGCAGAAATCACCACCTCTTGATCGCAGCAAAAGAAATATCATTGG
ATATTTTGAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCGAATATTTTGCA
TGATGATGTGCCCTTCTTTCTGCATTGGGGATGTTTCAAACCGGAAAGATATAGTGCGCA
CAACATAATCTACAAACCACCGGGCATTCTGCTCCGGATATGGTGTACTTGGGAGCTATGAC
AAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTTGTCGAGAAATAAC
ATTTGAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCATACTCTTTCACATGAA
AGAAGATACAGAAAGTTTAGAATATTTCCAGAATGAAGTAGCTCGGCAATTAATAAGTGAAAA
AGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACATCCTCTTCTGCACATACA
GAAAACCTCCAGCAGATTGTCTGTAAATCGCTATTGACAGCTTTAGGCATATGTATGTGTTTGG
AGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTCGTATTTGACTTACATTCTGG
AAAACCTGCACAGAGAATTCATCATGGACCTGACCCAACTGATACAGCCCCAGGAGAGCAAGC
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAAAACCTAGCACCAGTGAATATAG
GTATACTCTATTGAGGGATCGAGATGAGCTTTAA~~AA~~AACTTGAAAAACAGTTTGTAAGCCTTTC
AACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTATATTTTCATAATTCTATGTGTAT
TTTTATTTGAATAAACAGAAAGAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 430

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRESQM
LHPIFEAEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMCREYRGQ
RSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILHDDC
AFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREITFEN
GEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP
ADCPVIAIDSRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPGEQAQDV
ASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

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FIGURE 431

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGCA
GGCTGGCTGCTGCTGCTGCTTCCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAAGTGCGCGCCGGGCGTG
GACGCTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGCAGTG
CGGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCCTGGATCTTCACGGGCTTCTG
GCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTCACCTCG
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGCTATACCCGCCCAACGGCGTGGAGTGCTACAGC
TGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCTGTGAGCTGCTACAAC
GCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCAGCTAATGTG
ACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGATGGAGTAACA
GGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACCTCTGACCTCCGC
AACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCGGGTGCCCTCCAGAGCCACG
ACTGTGGCCTCAACCACATCTGTCAACCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACC
ACCAAACCCATGCCAGCGCCAACCAAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCCTCC
CGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGACCGCAGCAATTACGGG
CAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCACAGCT
GGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTGAAGCTTCTCCACCTGGA
AATTTCCCTCTCACTACTTCTCTGGCCCTGGGTACCCCTCTTCTCATCACTTCTGTTCCCA
CCACTGGACTGGGCTGGCCAGCCCTGTTTTTCCAAACATCCCCAGTATCCCCAGCTTCTGC
TGCCTGTTTTCGGGCTTTGGGAAATAAAATACCGTTGTATATATTCTGCCAGGGGTGTTCTA
GCTTTTTCAGGACAGCTCCTGTATCCTTCTCATCCTTGCTCTCCGCTTGCTCTTGTGATG
TTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTGAGAGAGAGGATGCTAAGCTTCC
TACTCACTTTCTCCTAGCCAGCTGGACTTTGGAGCGTGGGTGGGTGGGACAATGGCTCCCC
ACTCTAAGCACTGCCTCCCTACTCCCCGCATCTTTGGGGAATCGGTTCCCCATATGTCTTCC
TTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTACCCAATTTCGCCCTATAGTGAGTCGTA

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FIGURE 432

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCTE
AVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRALDP
AGNESAYPPNGVECYSCVGLSREACQGTSPFVVCYNASDHVYKGCDFGNVTLTAANVTVSLP
VRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTTVAST
TSVTTSTSAFVRETSTTKPMPAPTSQTPRQGVHEASRDEEPRLTGGAAGHQDRSNSGQYPAK
GGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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FIGURE 433

CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCCATGGAGTT
GGTGCTGGTCTTCTCTGCAAGCTGTGGCCCCCATGGTCTGGCCAGTGCAGCTGAAAAGGA
GAAGGAAATGGACCTTTTCATTATGATTACCAGACCTGAGGATTGGGGGACTGGTGTTCGC
TGTGTCCTCTTCTCGGTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTTTCAA
TCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACCGCCAATGC
AACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAACCTGAG
GCGGCTGCTTGAACCTTTGGATGCAAAATGTCGATGCTTAAGAAAACCGGCCACTTCAGCAACA
GCCCTTTCCCGAGGAGAAGCCAAGAAGCTTGTGTCCCCACCCCTATCCCCCTCTAACACCATT
CCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCGGTCTGCCACCTC
CCGTGATGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTGGTCTTTGTGG
CTACTTGTGTTGTGGATGTTATTGTGTTGTGTAGTGAAGTGTGGACTCGCTTTCCAGGCGAGG
GCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCCGTGGCCCTCCATCACCTTCTGCTCCTA
GGAGGCTGCTTGTGCCCCGAGAGCCAGCCCCCTCCCTGATTTAGGGATGCGTAGGGTAAGAGC
ACGGGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCACTTTGTATCATTTCT
TCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCCTTATCCCACCTGATCCCAGTCT
GAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCCAGCGTTGACGTCAGG
CAGGCTATGCCCTTCCGTGGTTAATTTCTTCCAGGGGCTTCCACGAGGAGTCCCCATCTGCC
CCGCCCTTTCACAGAGCGCCCGGGGATTCCAGGCCAGGGCTTCTACTCTGCCCTGGGGAAT
GTGTCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGGGACCTTACCCCTTCCAACC
TTCCCTGCTTCTGAGACTTCAATCTACAGCCAGCTCATCCAGATGCAGACTACAGTCCCTGC
AATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCCGTTGGGGCCAGCACCCGGGA
TGGATGGAGGGAGAGCAGAGGCCCTTGCTTCTCTGCCTACGTCCTTATAGATGGGCAGCAGAG
GCAACTCCCGCATCCTTTGCTCTGCCTGTGGTGGTCAGAGCGGTGAGCGAGGTGGGTGGAG
ACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAGGTTGAAGGTCAACAGAGAGTGGG
AACTCAACCCAGATCCCGCCCCCTCCTGTCTCTGTGTTCCCGCGGAAACCAACAAACCGTGC
GCTGTGACCCATTGCTGTTCTCTGTATCGTGATCTATCTCAACAACAACAGAAAAAGGAAT
AAATATCCTTTGTTTCCT

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FIGURE 434

MELVLVFLCSLLAPMVLASAAEKEKEMDPFFHYDYQTLRIGGLVFAVVLFSSVGILLILSRCKC
SFNQKPRAPGDDEEAQVENLITANATEPQKQRTQVQPSGGSLWNLRRLLEPLDANVDA

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FIGURE 435

GGTCCTTAATGGCAGCAGCCGCCGTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCCTCACTCTCTTTGTATGACATCACCGTCA
TCCCTAAGTTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCTGGGGAAGAAACTAA
ATGTCAACACGGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCA TTCACTGCCTTGATTCCCTTTTGCCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTCTTTTGTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTCCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

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FIGURE 436

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFLLH
YDCGNKTVTPVSPLGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAFLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

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FIGURE 437

GTTCCTCCTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAGCTCTTGTGGCAGG
TAACCTGTGCACCAACACACCTGGAAATGCCATCCTGCTCCCGTTGCTCTACCTCACGGCGCAAGTGTGGATTCTGT
GTGCAGCCATCGCTGCTGCCGCCCTCAGCCGGGCCCCAGAACTGCCCTTCCGTTTGCTCGTGCAGTAACCAAGTTCA
GCAAGGTGGTGTGCACGCGCCGGGGCCCTCCGAGGTCCCGCAGGGTATTCCTTCGAACACCCGGTACCTCAACC
TCATGGAGAAACAATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACACCTGGAGGTCCTGCAGTTGG
GCAGGAACCTCCATCCGGCAGATTGAGGTGGGGCTTCAACGGCCCTGGCCAGCTCAACACCTGGAGCTGTTG
ACAACCTGGTGACAGTCATCCCTAGCGGGCCCTTGAATACCTGTCCAAGCTCGCGGAGCTCTGGCTTCGCAACA
ACCCCATCGAAAGCATCCCTCTTACGCCCTTCAACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGAGCTCA
AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAAGGGCTGTTCACACCTCAAGTATCTGAACCTTGGGATGTGCA
ACATTAAAGACATGCCCAATCTACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACTTCCCTG
AGATCAGCCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTGATGAACACAGGTCAGCCCTGA
TTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACCTCAACTTGGCCCAACAATAACCTCTCTCTTTG
CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTG
ACATCTGTGTGGCTAGCCTGCTGGCTTCGAGAGTATATACCCACCAATCCACCTGCTGTGGCCGCTGTCATGCTC
CCATGCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAAGCCCTCCTTCCAGTGTCTGCCCCCTTCATCATGG
ACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAAGCTTAAGTGTGCGACTCCCCCTATGTCTCCG
TGAAGTGGTGTCTGCCAATGGGACAGTGCTCAGCCACGCCCTCCGCCACCCAGAGATCTCTGTCTCAACGACG
GCACCTTGAACATTTTCCACAGTGTGCTTTCAGACATGGGGTGTACACATGCATGGTGACCAATGTTGACGGCA
ACTCCAACGCCCTCGGCCCTACCTCAATGTGAGCAGGGCTGAGCTTAACACCTCCAACACAGCTTCTTACCACAG
TAACAGTGGAGACCACGGAGATCTCGCTGAGGACACAACGCGAAAGTACAAGCCTGTCTTACCACAGTCCACTG
GTTACCAGCCGGCATATACCACCTCTACCAACGGTGTCTATTGAGACTACCCGTGTGCCCAAGCAGGTGGCAGTAC
CCGCGACAGACACCCTGACAAGATGCAGACAGCCTGGATGAAGTCATGAAGACCACCAAGATCATCATTGGCT
GCTTTGTGGCAGTGACTCTGCTAGCTGCCGCCATGTTGATTGTCTTATAAACTTCGTAAGCGGCCACAGCAGC
GGAGTACAGTCACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGCAG
CAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGCGAGTAGTGCTGCCACAATTCATGACCATAATTAAC
ACAACACCTTACAACACAGCAGATGGGGCCCACTGGACAGAAACAGCCTGGGGAACCTCTCTGACCCCCACAGTCA
CCACTATCTCTGAACCTTATATAATTAGACCCATACCAAGGACAAGGTACAGGAAACTCAAATATGACTCCCT
CCCCAAAAAATCTATAAATGCAATAGAAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTT
TCTCTGTATATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTTAAATTTAAGACAAAA
AGTCAAAACA

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FIGURE 438

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAATAAAASAGPQNCPSVCSCSNQFSKVVCTR
RGLSEVPQGIPSNTRYLNLNENNIIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLN
TLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISE
GAFEGLFNLKYLNLMGMCNIKDMPNLTPLVGLEELEMMSGNHFPFIRPGSFHGLSSLKKLWVMNS
QVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDCDILWLAWWL
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP
MSSVKWLLPNGTVLSHASRHRPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSNASAYLNV
STAEINTSNYSFFTTVTVETTEISPEDTTRKYKPVFTTSTGYQFAYTTSTTVLIQTTRVPKQV
AVPATDITDKMQTSLDEVMKTKIIIGCFVAVTLLAAAMLIVFYKLRRHQQRSTVTAARTVE
IIQVDEDI PAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWNTENSLGNSLHPT
VTTISEPYIIQTHTKDKVQETQI

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FIGURE 439

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTG
TCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGC
CCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAA
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTGCACC
GATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAAATAGTAAAAAAT
GTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTCCAAAGTCTTTCAACGACACCCTGATC
TTCATAAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 440

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEVK
HCTDQISFKKRLSLKKSWWK

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FIGURE 441

GAACATTTT TAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG
GGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC
ACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGG
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAG
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAA
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGAAGGGC
AGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGTCAGGGGT
TCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGGGAAGAGGC
CAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAAGCCTTACTCACCTCTCTCTAAGTTTAGA
AGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGG
AGGCGAATAAATGTTCAAACGTGA

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FIGURE 442

MPSPGTVCSELLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG
QAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 443

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTCG
TGAACCCCGGGTGCTCCGCACGGACCCAGATGTCAAGAAATATGAACACGTGGCTGCTGTTCC
CTCCCCCTGTTCCTGGGTGCAGGTGCAGACCCCTGATAGTCGTGATCATCGGGATGCTCGTGCTC
CTGCTGGACTTTCTTGCTTGGTGACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT
ATGTCCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATCTTACAA
CCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCAGCCTGGGGCCAGAGTCTTTGTCCTCC
CGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAAGGGCAAA
TCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCCAGCAAGAAGCTGAACTCACGCCG
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTACAGACAATGGA
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAAACAC
AAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCACCCACTAACCAACAACCTGAAG
CGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTGAGTCATGTTGCT
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGTAACAACAACCTCC
CTGCTCCTGGCACCAGCCGTTTGGTTCATGGTGGGCCAGCTGCAAAGCGTCTTCCATTCTCTG
GGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGACACGGGCAGCAGAGTG
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCAACCCCTGGTCAGGGCA
GAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGAGCATCCCCTGCCTGCAG
TTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGAGCCTCCTTGTTTATAAACC
ACAGGTTACCCCTACAAACCCTGTCCCCACACAACCCCTGGGGATGTTTTTAAACACACACCTC
TAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGAATTTTTTTTAAATGAAAGTGC
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

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FIGURE 444

MNTWLLFLPLFPVQVQTLIVVFI GMLVLLLD FLGLVHLGQLLI FHIYLSMSPTLS PRSPQGWV
VRAAHLTPLLEYVPNPEPFTPGARVFVPRVRMCSGASPRSEIMDKKGKSQEEIKSMRTQQAQ
QEAELTPRPAGVVPGA

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FIGURE 445

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTGC
TGTTTCTTCTTACCATTTCATCTTCTCTGGGGCTGGGCCAGCCAGGAGCCCAAAGCAAGA
GGAAGGGGCAAGGGCGGCCTGGGCCCTGGCCCTGGCCCTCACCAGGTGCCACTGGACCTGG
TGTCACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG
CCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCTGTGGA
TGTCACAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCCGTATCC
CCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACCATGCAGG
AGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCGCTCTGCC
CGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCT
GCACCTGCATCTTCTTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGACCATCCTCCT
TGCACCTTTGTGCCAAGAAAGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

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FIGURE 446

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGGGRPGPLAPGPHQVPLDLVSRMKPYARMEEYE
RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCLGC
VNPFTMQEDRSMVSVFVSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

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FIGURE 447

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAGA
TGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT
CACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGGTGC
CCAAGCCCCGTGTGCGAGAAAGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCTCGGATG
GAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGACCGGT
TCTCCTTCGGAGCTTCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAGAACCAG
GGGAGAGGTGCCAAGTTTCATTGAACCTTACACCACCAGCCAAGAGAGGTGAGAAAGGACTAC
TGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAAGCGGTTGA
TGGAGAAGGCTTCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTATGGTTATCC
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCACTCAGCTTCTCCTGCTACTAACAGAC
TTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGTGCTGTTTCTCTCT
GTCCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTCTTCCAAGCGACT
GTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATATGGCTGGGCCTTCTACATG
GCCTGGCTCTCCTTCACTGCTGCATGGCGTCGGCTGTCAACACCTTCAACACGTACACCAGG
ATGGTGCTGGAGTTCAAGTGCAAGCA**TAG**TAAGAGCTTCAAGGAAAACCGAACTGCCTACCA
CATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGACCCCCACCGTGGGTCTTTTGACC
AGCTACCACCACTATCATAATCAGCCCATCCACTCTGTCTCTGAGGGAGTCGACTTCTACTCC
GAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA
TCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGAGTAGGCTTGAGCCCTACCT
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGTCTCTTGAGCATGGTTTTTA
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTCTTAAGGGATTCTCGGGTGCCA
CTGCTCTCTTTCTCTACAGCTCCATCTTGTTTCAACCACCCACATCTCACACATCCAGAA
TTCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGCTAAACCATGGAGATAAAAAGAAG
AGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 448

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMPV
SLDGDNTNTSTQEVVQYNWETGDDRFsFRsFRSGMWLSCEETVEEPGERCRSFIELTPPAKRGE
KGLLEFATLQGPCHPTRLRFGGKRLMEKASLPSPLGLCGKNPMVIPGNADHLHRTSIHQLP
TNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLTTCLLELWLG
LLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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FIGURE 449

CCGCAGCGGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCC
 ACGCGTCCGGTGCAGGCTCCGCCCGCACACTGCCTGGTGGAGGGAAGGAGCCCGGGCGCTCTCGGCCGCTCCGCC
 CGCGCGCTCCGCCAGCTCCCGACCGCCGCCGCCCGCGCGCGGCGGAAAGCTGAGTGAGCGCCGCTCTCT
 GCAGCGTCCGCCGGGGCGCGAATGGCAGGCTGTTTCGCGGAGTAAAGAGTGGCGCGGTCAGTGGTCTGTTCCAAAT
 GACGGCATTTAACCAAGTCTGCAGATCTCGGGGAGTCCGACCGCCGACTTGGAGATTTCCTCCCGCACAACT
 CAGAGTCCGAACTGCAGAGCAAGAGAAAGCGGAGCAAGCTCGCGTCCGCCAGCTATGGGAACT
 TGGCGGCTCTAGAAATTCGCTCCGCCCTTCGCCGGCGCCCTTCGACGCGCGAGCGGAGCAAGAAATGAGACAT
 TGCGCGCTCCGCAGATCGCGCGCGCGGAGCGGGGCTGCCTCGGAACACAGAGGGGTCTTCTCTCGCCGTCGA
 TATATTAGGCTGCACACAAAGGACGAGCTGAATGGAGTGTGCTACTCTCGGAAAGGATTTCTGACCGAGCGC
 TCTCCAAATGACATCTCTCAAGTCTCTCTCGGAAAGATTCTCGTAAATGATTTCGCTGCTCTGCTGTCTAT
 ACTGGCTGCTGAGGAGGGCCCTCGGGGTGGTCTTGCTGCTGCTGGGGGCTGCTTTCAGATGCTGCCGCCGCC
 CCAGCGGGTCCCGCAGCTGTGCCGTGGGAGGGGGGCTGCTGTACTGGGAGGCGCTCAACTCCACCGAGGGCG
 CCCACAACTCTCCGGGCTGTCTGGGCTGTCTCCCTGCCTACAAAGCTCTCGGAGCTCGCGGGCGGCCATTTCA
 CGGGCTTAATGTCAGCTCTACGTGGCTCTATCTGGATCAATCAATCAATCTGCTCGCGAGGGGAGCTCTTGA
 AACTGCGCGAGTTAAGAACTTCAGCTTGTCTTCAACAGATCACTCACTGCCACACCACTCTCCGCCCA
 TGCACAACTCCGAGCTGGACCTCTCTGACAAACAGCTGCAAGGCGCTCGCGCGCGACCTCTTCCAGGGCTG
 GGAAGCTCACCCAGCTGCATATCGGGGCCAAGCCATCCAGTTTGTGCCCTGCGCATCTTCCAGGACTCCGCA
 GCTCAAGTTTCTGACATCGGATACAATCAGCTCAAGAGTCTGGCGCGCAACTCTTTCGCCGGCTTGTATTAAGC
 TCACCGAGCTGCACCTCGAGCACAAAGGACTTGGTCAAGGTGAATTCGCCCACTTCGCCGCTCATCTCCCTGC
 ACTCGCTCTGCTCGCGGAGGAAACAGGTGGCCATTTGGTCAGCTCGCTGGACTGGGTTTGGAACTCGGAGAAAA
 TGGACTTGTGGGCAACGAGATCGAGTACATGGAGGCCCATGTGTTTCGAGACGCTGCCGACTCGAGCTCCGTCG
 AGCTCGACTCCAACTCTCACTACATCGAGCGCGGGATCTCACTCTTTGGAGTCTCGAGCTCCGACGATCACTC
 TGGCGGGAACCTTGGGATTTGGGGGCAAGCTGTGTGCCCTAGCCCTGCTGCTGAGACTTCAGAGGAGCGCT
 ACGATGGCAACTTGCAGTGGCGGAGTACGCAAGGCGAGGAGCTCTGGAGCGGCTGAGCGCTTCC
 ACTGTGCGAGAGTGGGGCGGAGCCACAGCGGCCACCTGCTCTCGGGCTGACCAACCGGAGTATCTTGGGGC
 CCCCCTCGAGCTCGGCCACACGCTCGCGGAGCGCGGGGAGGGGAGCAGCAGGAGCACTTCGAGCTCTGCCACG
 TGGCTCTTCCAGCGGGGAGCACTCGCGGAGCGCGCTGCAAGTCCCAAGGTGGTCAAGGGACCATCGGCCCTCA
 TCTCTCTCTCTCTATCGTGTGCTCTGCTGTCTGGAAGTGTTCGCGAGCGCTCAGGCACTCA
 GACAGTGTCTGTGTCAGCGAGCGAGGAGCAAAAGCAGAAACAGACCATGATCAGATGGCTGCCATGTCTGCC
 GAGGATACAGCTGATTCACAAACGAAACATTTGGGAGCGCTCTGTATCATCAAGCATTTGGCTGTCTA
 CCGCGCAAGCTTACCTACATCACTTATGCCCTGCTGCTTGTGCTGAGATTTGCTGGGAGGTGGGGGAGGTGGGGGA
 AACGGCAGGAATAAGGGAAAGTGGTAGTTTAACTAAGGTTTGTAACTATGAAATCTTTCTTCTCAAAATTA
 ATTAATCTTAAAGCTTCAAGAACTTGTCTGACCCCTCTAAGCAACTACTAAGCATTTAAAGAGAGATCTAATT
 TTTAAAGGTGTAGCACTTTTGTATTTTATCTTCCACAGAGGCTGCTAATCTATTATGCTGTGCTATCTGAAAA
 GAACTTAAGGCCACATCTCAAGTCTCGTCTGGGCAATGTGATGGATTGACCTTCCATTTGCAGTACCTTCCAG
 CTGATTAAATTCAGAGTGGTATTTGAGGTTTTTTCGAATATTTATATAGAAAAAAGTCTTTTACATGACAAAT
 GACACTCTCACACAGTCTTAGCCCTTAGTAGTTTTTGTAGTGGACAGAGGAAGCAGGTTTAATGAGACTGTC
 CTCTCTGCTCAAGAAATACGAGCTCCCTGATGTCGATTTGCTGCTGATTTGCTGATTTAATGATTTAGCAGC
 TACCCACATGCACTTATCTCCAGAGCTCAAAATTTACATCGGAAAGGAAGGTATTTCACAAAGAGAA
 ATAGTTTCTCAACCATTTAAATATTTCTTCTGAATCATCAAGTAGAAGGCCCACTCTTTCTCTCTGTC
 CTCAAGAAAGGCAGCATTTGGTATGATTTAGCATCAACAAACATTTATAGTATATGTAAGTAAACAGAGGGG
 CAAATGCCACTTGTATTCTCTCCCAAGTTTCCAGCAAGTACACACAGATCTCTGGTAGGATTAGGGGCGACTT
 GTGTTTCCGGCTTATTTTGTGCGACTTTCAGCAAGTTTGTAGCGTATCTATCTGACATGGCCGAGTGAACAG
 GGCATGTAGTATCATCAGATGTTGAGAAAGAACATCATCATACCTTCCATCAGAGAAATATTAAGAA
 CCAGAAATATATCTGTTTGGAGCAAGGTGTCAATGTTTCAGGGTAGTCAAAATAAACATTAATCTCTTC
 CTGATGAGTGAGGTGCTTGGCTGATTTGGGTCTGCAATGACAGATGTCAAAATAAGGAATAGGTAGTAGAA
 TATGACATTAATGATGCTCTGAATATATTTGAGATAGTTTGAATGTC

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FIGURE 450

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHN
LSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTISSNQIT
QLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRSLEK
LDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIVVSSL
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSITLAGNL
WDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCEDGAEPTSGHLLSAV
TNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLI
VVLVLYVSWKCFPASLRQLRQCFTVQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALV I
NEYGSCTCHQQPARECEV

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FIGURE 451

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCTCCAGTCACCCCTCCCGCGGTTAC
CCGCGCGCGCGCCCGAGGGGAGTCTCCTCCAGACCCCTCCCTCCCGTTGCTCCAAACTAATACGGGA
CTGAACGGGATCGCTGCGAGGGTGGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGACAACT
ACCATTCCATAGCCAGATAGATTATCTTACACTGAACTGATCAAGTACTTTGAAAATGACTTCG
AAATTTATCTTGGTGTCTTCTACTTGTGCTGCAC TGAGTCTTTCAACCACCTTTTCTCTCCAA
CTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACTTATATAAA
GTTCCAAACGCCCTTTTTCATTATATTATGAAATATGGTGTTACAGTGAAGCAAGTTACTAAT
GTTTTTATTACAAAACCTACCTAACCATTTACTTTGGTAACTGGCCTCTTTCAGAGAAAT
CATGGGATTGTTGCAAAATGATATGTTTGATCCTATTTCGGAACAAATCTTCTCCTTGGATCAC
ATGAATATTTATGATTCCAAGTTTTGGGAAGAAGCGACACCAATATGGATCACAAACCGAGG
GCAGGCATACTAGTGGTGCAGCCATGTGGCCCGGAACAGATGTAAAATACATAAGCGCTTT
CCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAGAGTTGCCAAAATTGTT
GAATGGTTTTACGTCAAAAGAGCCCATAAAATCTTGGTCTTCTCTATTTGGGAAGACCCGTGATGAC
ATGGGGCCACCATTGGGGACCTGACAGTCCGCTCATGGGGCCTGTCATTTTCAGATATTGACAAG
AAGTTAGGATATCTCATCAAAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATC
ATCAGAGATCATGTGAATGACGCGAGTCTGTGAGGAAAGGTTAATAGAACTTGACCGATAC
CTGGATAAAGACCACTATACCCTGATTGATCAATCTCCAGTAGCAGGCATCTTGCCAAAAGAA
GGTAAATTTGATGAAGTCTATGAAGCACTAACTCACGCTCATCTAATCTTACTGTTTACAAA
AAGAAAGACCTTCCAGAAAGGTGGCATTACAAATACAAACAGTCGAATTCACCAATCATAGCA
GTGGCTGATGAAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACCAC
GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCTCGCTTCAG
AAGAATTTCTCAAAAGAAGCCATGAACTCCACAGATTTGTACCCTACTATGCCACCTCTC
AATATCACTGCCATGCCACACAAATGGATCATTTCTGGAATGTCCAGGATCTGCTCAATTCAGCA
ATGCCAAGGGTGGTCCCTTATACACAGAGTACTATACTCCTCCCTGGTAGTGTTTAAACCGACA
GAATATGACCAAGAGGGGTCTACCCCTTATTTATAGGGGTCTTCTCTTGGCAGCATATAGTG
ATTGTATTTTTTGTAAATTTTCATTAAGCATTTAATTCACAGTCAAATACCTGCCCTTACAAGAT
ATGCTATGCTGAAATAGCTCAACCATTATTACAAGCCTAATGTTACTTTGAAGTGATTTGCAT
ATTGAAGTGAGATTCCATAATTATGTGAGTGTTTAAAGGTTCAAATCTGGGAAACCGATT
CCAAACATCTGCGAGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACAC
CACATACACACACACGACCAAAAATACTTACACCTGCAAGGAATAAAGATGTGAGAGTATGT
CTCCATTGTTCACTGTAGCATAGGGATAGATAAGATCCTGCTTTATTTGGACTTGGCGCAGAT
AATGTATATATTTAGCACTTTGCACATATGTAAGTACCTTATATATTGCACTTTAAATTTCT
CTCCTGATGGGTACTTTAATTTGAAATGCACCTTATGGACAGTATGTCTTATAACTTGATTG
AAAATGACAACCTTTTTGCACCCATGTACAGAATACTTGTACGCATTGTTCAAACCTGAAGGA
AATTTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATGAGAGAAGAGAA
GGTGATAAGTGTGAAAATTAATGTGATAACCTTTGAACCTTGGAGATTTGGAGATGTTATCC
CAACAGCAGAATGCAACTGTGGGCATTTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTCA
TTTATTTTTCCCTCAAAAGAGAGTCAAAATCTGACAGATTCTGTTCTAATATATTTGTTTCTGT
CATAAAATTTATGGATTTCCGTGATGAGTCATATTACTGTGATTTTCATAATAATGAAGACAC
CATGAATATACTTTTCTTCTATATAGTTCAGCAATGGCCTGAATAGAAGCAACCAGGCACCAT
CTCAGCAATGTTTCTCTTGTGTAATTTTGTCTCTTTGAAAATTAATCATTAAAT
ACATTAATAATCAATTTGGATAAAAAAAAAAAAAAAAAA

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FIGURE 452

MTSKFILVSFILAALSLSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVKQ
VTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPINRKSFSLDHMMNIYDSKFWEETPIWIT
NQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLYWED
PDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTNLNIITS DHGMTQCSEERLIEL
DQYLDKDHXYTLIDQSPVAAILPKEGKFDEVYEALTRAHPNLTVYKKEDVPERWHYKYNRIQP
IIA VADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTDLYPLLC
HLLNITAMPHNHGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPFYFIGVSLGS
IIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Important features:**Signal Peptide:**

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,
382-385, 389-392**Somatomedin B Domain:**

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

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FIGURE 453

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGAC
T**ATG**GGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTGCT
GATGGCCGCCTGCTTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGGCCCTGACCAA
CCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGAGCTGGA
TGCCGAAGTCTCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGGCAGGC
TGTCCCTGCAGGATCCACGTCACGGCTGAATCTTCAGACTGGGGAAGAGAGGCCAAAACCTCCA
ATATGAGGACAAGTTCGAAATAATTGAAAGGCAAAAGGCTGGATATCAACACCAACACCTA
CACATCTCAGGATCTCAAGAGTGCACCTGGCAAAATTCAAGGAGGGGGCAGAGATGGAGAGTTC
AAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGAGGAACGAA
GAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGGTACGGCTGAT
CAACAAGTTCAATAGTTCCAGCTCCAGTTTGGAAAGAGAAGATGCTGCGCTCTTTGATCTTGA
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGGTCTTCAAGTGGT
GATCAATGGGCTGAACAGCACAGAGCCCCCTCGTGAAGGAGTATGCTGCGTTTGTGCTGGGCGC
TGCCTTTTCCAGCAACCCCAAGTCCAGGTGGAGGCCATCGAAGGGGGAGCCCTGCAGAAGCT
GCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGTCTGTTTGCACCTGTG
CTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCTCGAAGCTCGGGGGGCTGCAGGT
CCTGAGGACCTGGTGCAGGAGAAGGCACGGAGGTGCTCGCCGTGCGCGTGGTCACACTGCT
CTACGACCTGGTACGGAGAAGATGTTGCGCGAGGAGGAGGCTGAGCTGACCCAGGAGATGTC
CCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAGGCCCTGTGGGAACAGGGCTG
GTGCGAGATCACGGCCCACCTCCTGGCGCTGCCCAGCATGATGCCCGTGAGAAGGTGCTGCA
GACACTGGGCGTCTCTGACCACCTGCCGGGACCGCTACCGTCAGGACCCCCAGCTCGGCAG
GACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCAGCCTGGAGCTGCAGGATGGTGA
GGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAACAGCTTGTGAAGGAGCTGAGAT**G**
AGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGAGGCTGAGGGGTGCCAGCGTGGGTG
GGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCTTGGCCATTAAATGGAAACCTGAAGG
CCAAA
AAA

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FIGURE 454

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNP EKSSSTKETERKETKAE EELD
AEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTY
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVRLI
NKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAEVLGA
AFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKGGGLQV
LRTL VQEKGTEVLAVRVVTLTYDLVTEKMF AEEEEAE LTQEMSPEKLQQYRQVHLLPGLWEQGW
CEITAHLLALPEHDAREKVLQTLGVLLTTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE
DEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

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FIGURE 455

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAGT
GGCCAGGAAGGCACAGGCCTGAGAACTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCTA
CCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGGTGT
CTGTGCGTCTCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCTAGAC
TCCTATCTTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGTCTTTG
TGGTTCTCTCTACCTGGGGAATAAGGTGCAGCGGCCCATGGGCTACAGCAAGACCCCCCTGGA
TGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGTCACAGAGCATGTTCTCGCCA
ACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG
GAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCAATGGATCCG
ACTGCCATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAACCAGCTCTACT
GCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAGGAAGAAAGTTT
TCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGCAGCAGATGTTCC
AGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCTAACGACCTCATGC
TCATCAAACCTGAACAGAAGAATTGCTCCCACTAAAGATGTGAGACCATCAACGTCTCCTCTC
ATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAAACAGAGCCCCCAAG
TGCACCTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGG
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACT
CCTGCCAGGGTGATTCTGGGGGCCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCTT
GGGGAGATTACCTTGTGCCCGGCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTCA
CCAAGTGATCCAGGAAACCATCCAGGCCAACTCTTGATGTCATCCAGGACTCAGCACACCGG
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAGACCTCATTCCTTCCAGAGA
TGTTGAGAATGTTTATCTCTCCAGCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCC
CCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCCTGGGAACAATTTCCAAAACCTGTCCAG
GGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCATCTCAAGCTCAGGGCCCATCCCTT
CTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGAAGTGGAAGAAAAAAA

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FIGURE 456

MATARPPMWWLICALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS
SSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAHCRKKVFRVRLGHYSLSPV
YESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRIRPTKDVRPINVSSHCP SAGTKCLVSG
WGTTKSPQVHFVKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGD SGGPVVCN
GSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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FIGURE 457

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCCTTTAGTGCCTTGCTTCCTGAAC
AGCTCAGAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCTCACCCTGTAGGAATCCAGATGCGAGG
CCAGTACAGCAGCAGGAGGACATGCTGGATGATGATGGGGACACCCATGAGCTGCATTTCTCAAGCCTCTG
CCACAACCTCGGCATCCAGAGCCCCGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCACTGGCCCTGA
CCCTGCTGACTTTTGTCTTGGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTCAGTACTACCAGC
TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAATCTC
TTCAAGTCCAGAATATAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTCGTGAGCTGTATAACA
AAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAAATGGAATGGCATGGAGACAATTGCTACCACTTCTATA
AAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAAC
AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCGC
CTGACAGTGGCAAGGCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAAGTGTCCATATTATAATAGATG
TCACAGCCCCAAGAAGCAGAGACTGTGTGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAAGAAATTGA
AGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCG
AAGGTGACTGGAATTCGCCCTCTGCACTACAAATAGCAGAGTGAGCCAGCGGTGCCAAAGCAAGGGCTAGTTGAG
ACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAATGGGTTCTCGTGTTTCTCTGT
CAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTACATGCCAC
CAACCAACCTCAGAAACCCATAATGTCACTGCTGCTTCTGGCTTAGAGATAACTTTTAGCTCTCTTCTCTCAA
TGCTAATATCACCTCCCTGTTTTCATGTCTTCTTACACTTGGTGGAAAGAAACTTTTGAAGTAGAGGAAA
TACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCCAGATTGTAC
CAGCAAAATACACAAGGAATCTTTTGTGTTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCC
CATCTGCCCTTGCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAACTCAAAATCTCAATGCCCTATAA
GCATTCCTCTCTGTGTCCATTAGAGCTCTGATAATTGTCTCCCTCCATAGGAATTTTCCCAGGAAAGAAATAT
ATCCCATCTCCGTTTCATATCAGAACTACCGTCCCGATATTCCTTCAGAGAGATTAAGACCAAGAAAGAGT
GAGCCTTCTCACTGCACCTGTAAATAGTTTCAGTTCCTATTTTCTCCATGACCCATATTTATACCTTTCAGGT
ACTGAAGATTTAATAATAAATAATGTAATACTGTGAAAA